

Blast Result

EXHIBIT 6



Blast 2 Sequences results

Entrez

BLAST

OMIM

Taxonomy

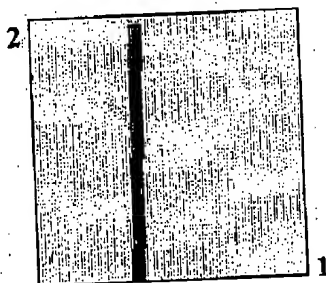
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

 Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 gi Homo sapiens endothelial differentiation, sphingolipid G- Length 1137 (1..1137)
 488..194 protein-coupled receptor, 3 (EDG3), mRNA

Sequence 2 lcl|s:q_2 Length 23 (1..23)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 44.9 bits (23), Expect = 0.17
 Identities = 23/23 (100%)
 Strand = Plus / Plus

Query: 423 caaaatgaggccttacgacgcca 445

Sbjct: 1 caaaatgaggccttacgacgcca 23

CPU time: 0.05 user secs. 0.13 sys. secs. 0.18 total secs.

Lambda K H
 1.33 0.621 1.12

Gapped
 Lambda K H
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 1

3/8/2002

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Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10:0: 1
length of query: 1137
length of database: 5,006,917,935
effective HSP length: 24
effective length of query: 1113
effective length of database: 4,991,889,975
effective search space: 5555973542175
effective search space used: 5555973542175
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)